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CTACTTCGCCAGCGTGAACTGGTTGACGTGCGATGTAGCCGACCCGGAACAGCTTGGCGCAGCCGGTCAGGTATTTTC
 ATGTACCGCTCGTAGACCTCTTCGGACTGGATCGCGATGGCCTCGCTTTTGTGTCTCTGCAGCGCCTCGGCCACAG
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 GATCGAGGAACAACGCGAAGAAAGTCATCCGAAATGTCGTAAGCCGACTGTGACTCTTCGTAATATGTTCTCAGCTT
 GGCCAT

Fig. 2: Sequence of *mmaA2* and *mmaA1* gene with an intergenic region of 166 base pair (shown in lower case. Location of forward A, sequence ID 1 and reverse primer D, sequence ID 2. Both primer sequence is underlined and italicized.

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1 2 3 4 5 6 7 8 9 10 11 12 13 14

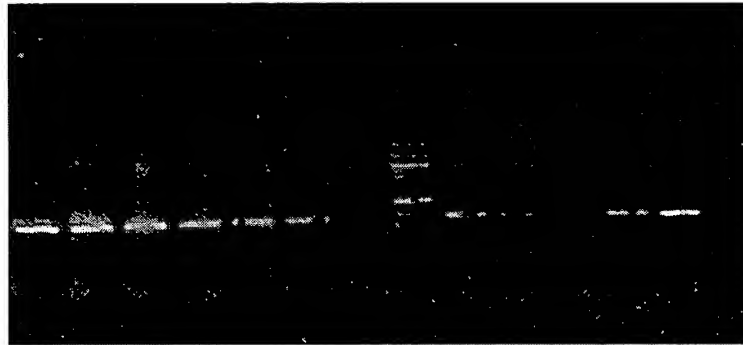


Fig. 3 PCR amplification of different mycobacterial genomic DNAs with primers A and D (lanes 1- 15): 1. *M.avium* 2. *M.bovis* 3. *M.chelonae* 4. *M.fortuitum* 5. *M.intracellulare* 6. *M.kansassi* 7. *M.phlei* 8. 100 bp DNA ladder 9. *M.marinum* 10. *M.scrofulaceum* 11. *M.smegmatis* 12. *M.szulgai*, 13. *M.tuberculosis* and 14. negative control. AD indicates 363 bp-amplified product.

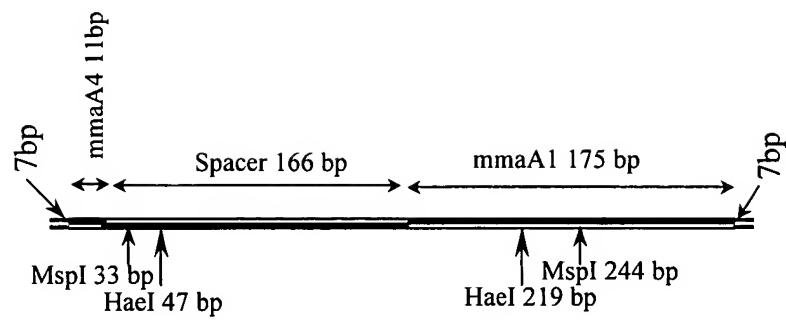


Fig. 4: line diagram showing restriction endonuclease map of HaeI and MspI within AD.

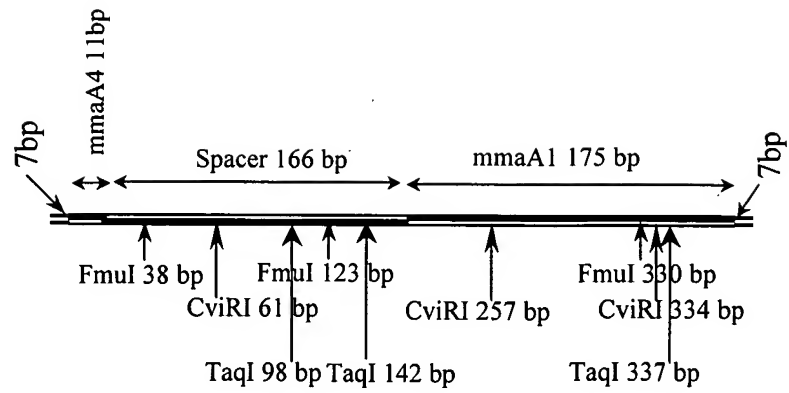


Fig. 5: line diagram showing restriction endonuclease map of Fmul, CviRI and TaqI within AD.

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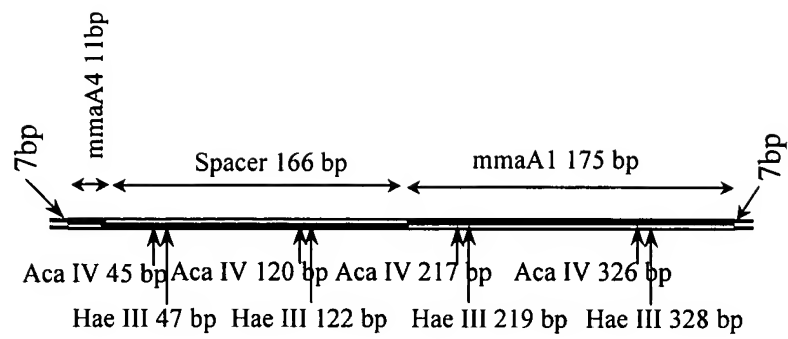


Fig. 6: Restriction map of AD showing distribution of the sites of restriction endonucleases AcaIV and HaeIII.

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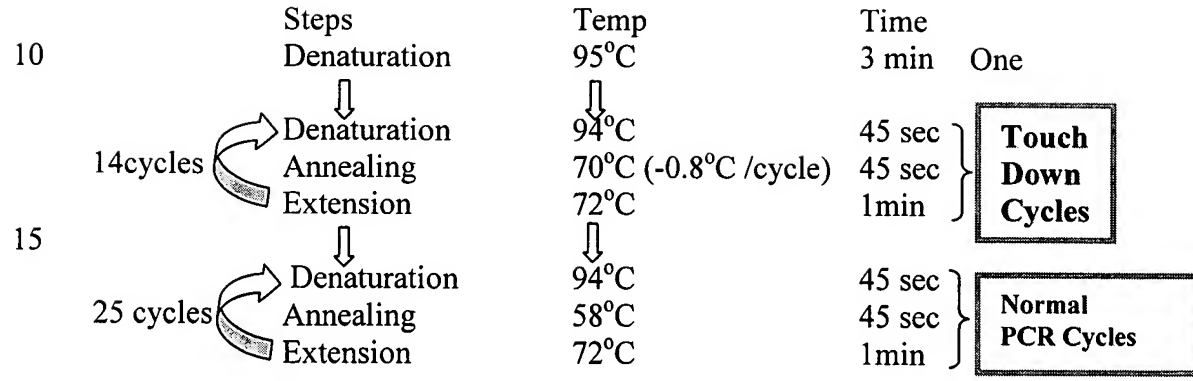


Fig. 7: Line diagram showing different steps of PCR reaction